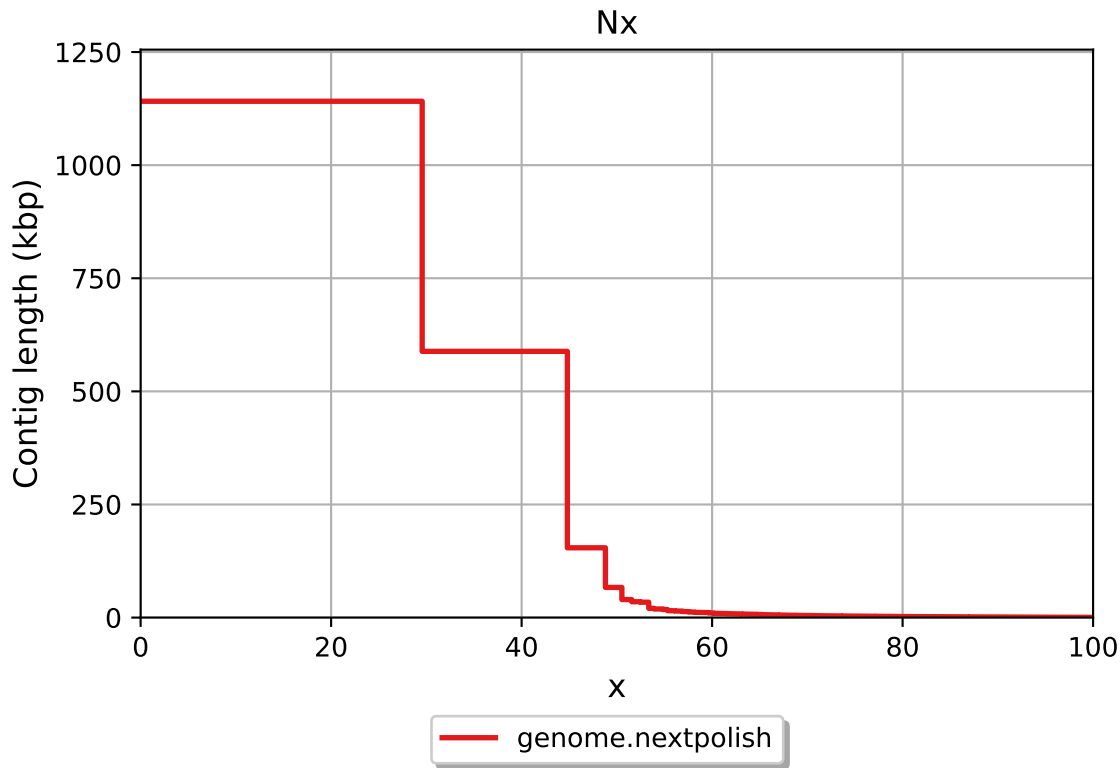
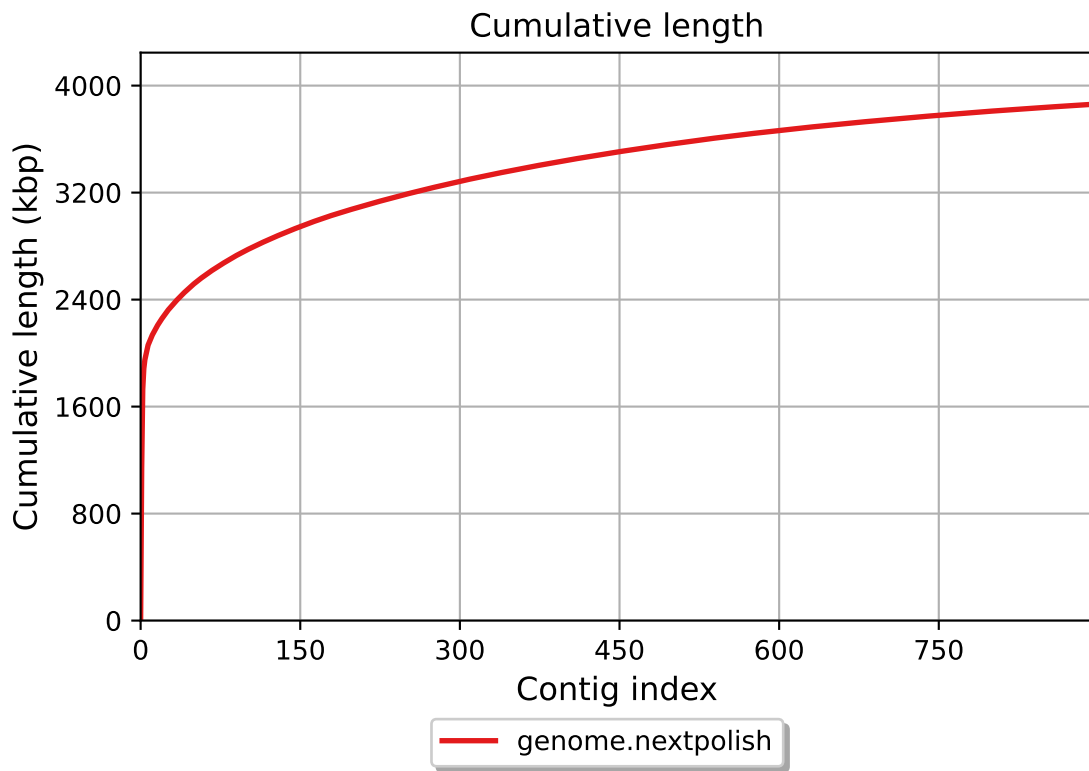


# Report

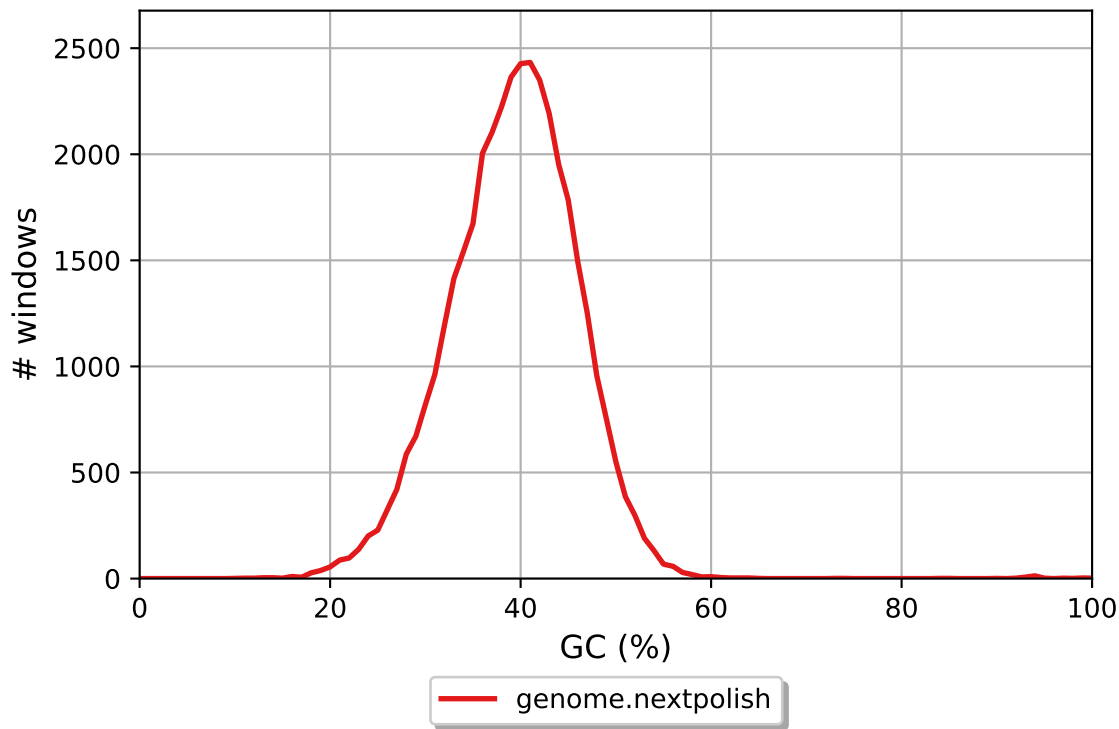
	genome.nextpolish
# contigs (>= 0 bp)	1722
# contigs (>= 1000 bp)	546
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	25
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	4127363
Total length (>= 1000 bp)	3614020
Total length (>= 5000 bp)	2653768
Total length (>= 10000 bp)	2313361
Total length (>= 25000 bp)	2059436
Total length (>= 50000 bp)	1950551
# contigs	895
Largest contig	1141184
Total length	3860477
GC (%)	39.24
N50	66670
N90	1313
auN	437651.5
L50	4
L90	426
# N's per 100 kbp	0.60
Complete BUSCO (%)	0.00
Partial BUSCO (%)	0.00
# predicted rRNA genes	21 + 1 part

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

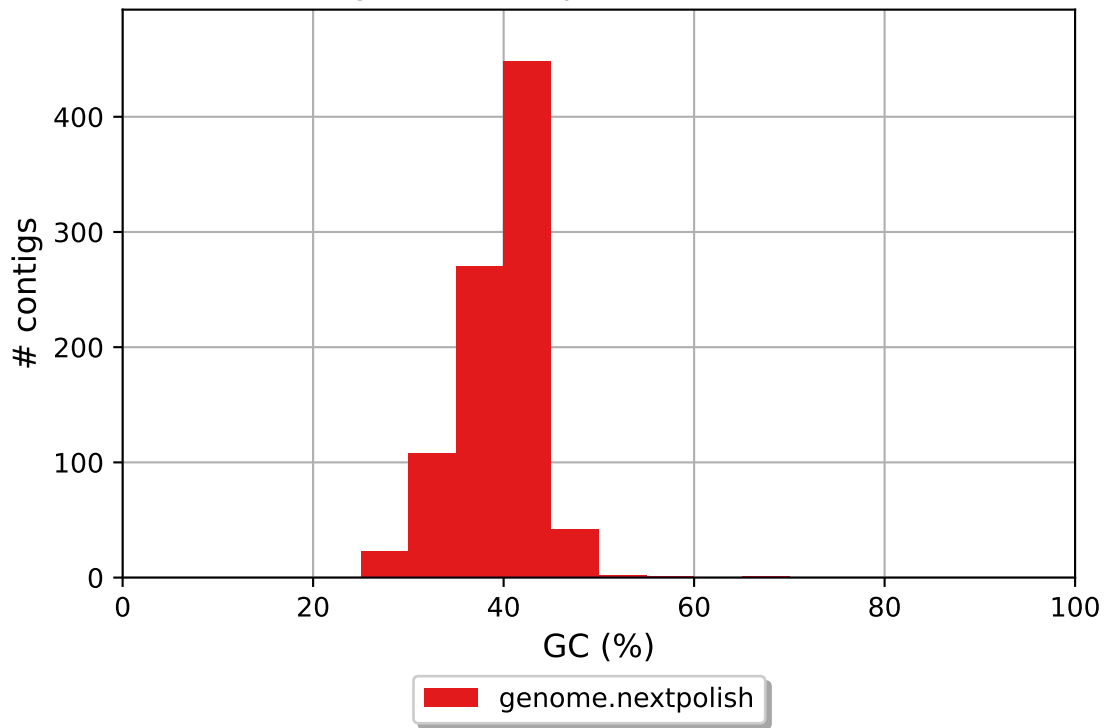




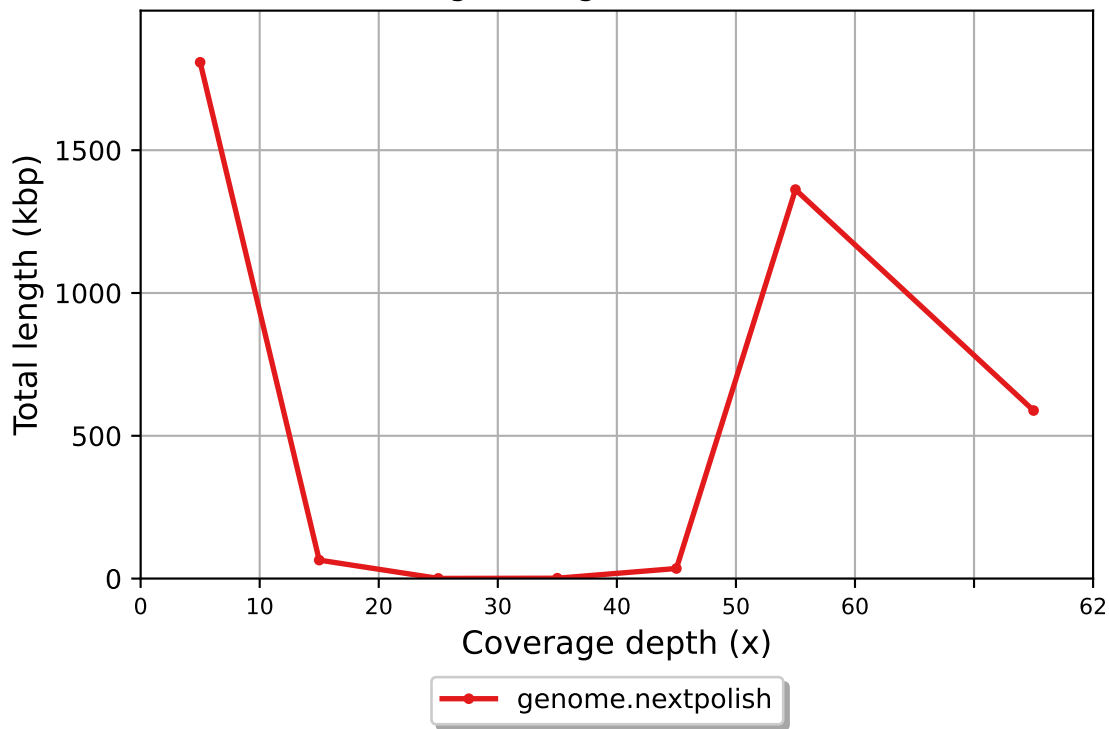
## GC content



genome.nextpolish GC content



Coverage histogram (bin size: 10x)



genome.nextpolish coverage histogram (bin size: 10x)

